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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:08 ; Search time 88.16 Seconds
(without alignments)
29.249 Million cell updates/sec

Title: US-09-331-631A-39

Scoring table: BLOSUM6DDX

Perfect score: 54

Sequence: 1 CXXXXCXXXXXXXXXXXXCXXXC 22

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15; *

1: sp_archaea; *

2: sp_bacteria; *

3: sp_fungi; *

4: sp_hexatrichous; *

5: sp_invertebrate; *

6: sp_mammal; *

7: sp_mhc; *

8: sp_organelle; *

9: sp_phase; *

10: sp_plant; *

11: sp_rhizarians; *

12: sp_virus; *

13: sp_vertebrate; *

14: sp_unclassified; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Length	DB ID	Description
1	54	100.0	39	Q9PVG7
2	54	100.0	43	Q9VUN2
3	54	100.0	44	Q9VUN2
4	54	100.0	46	Q9VUN2
5	54	100.0	46	Q9VUN2
6	54	100.0	47	Q9VUN2
7	54	100.0	49	Q9VUN2
8	54	100.0	49	Q9VUN2
9	54	100.0	49	Q9VUN2
10	54	100.0	49	Q9VUN2
11	54	100.0	57	Q9VUN2
12	54	100.0	58	Q9VUN2
13	54	100.0	59	Q9VUN2
14	54	100.0	62	Q9VUN2
15	54	100.0	66	Q9VUN2
16	54	100.0	67	Q9VUN2
17	54	100.0	68	Q9VUN2
18	54	100.0	71	Q9VUN2
19	54	100.0	72	Q9VUN2

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ALIGNMENTS

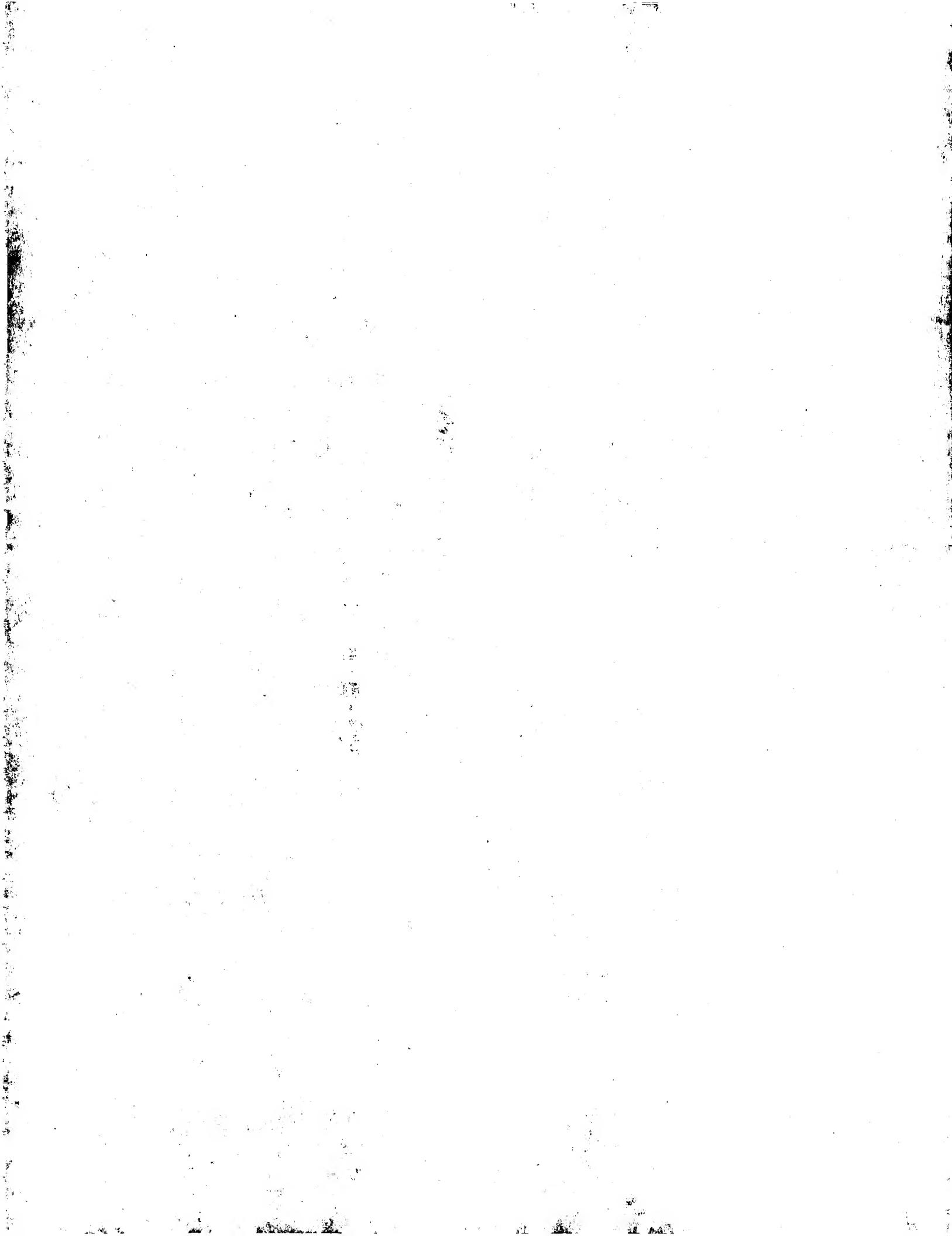
RESULT ID	PRELIMINARY;	PRT;	39 AA.
Q9PVG7			
AC	Q9PVG7;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE	RECEPTOR TYROSINE KINASE XMRK (FRAGMENT).		
GN	XMRK.		
OS	Xiphophorus maculatus (Southern platyfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii; Acanthomorpha; Acanthopterygii; Pecromorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.		
OX	NCBI_TAXID=8083;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SR;		
RX	MEDLINE=9912643; PubMed=9927468;		
RT	Gutbrod H., Schartl M.;		
RT	"Intragenic sex chromosomal crossovers of Xmrk oncogene alleles affect pigment pattern formation and the severity of melanoma in Xiphophorus".		
RL	Genetics 151:773-783(1999).		
DR	EMBL: AF092693; AAB03714.1; -.		
KW	Receptor; kinase.		
FT	NON_TER 1		
FT	NON_TER 39 39		
SQ	SEQUENCE 39 AA; 4195 MW; 42303BA05F6DB557 CRC64;		

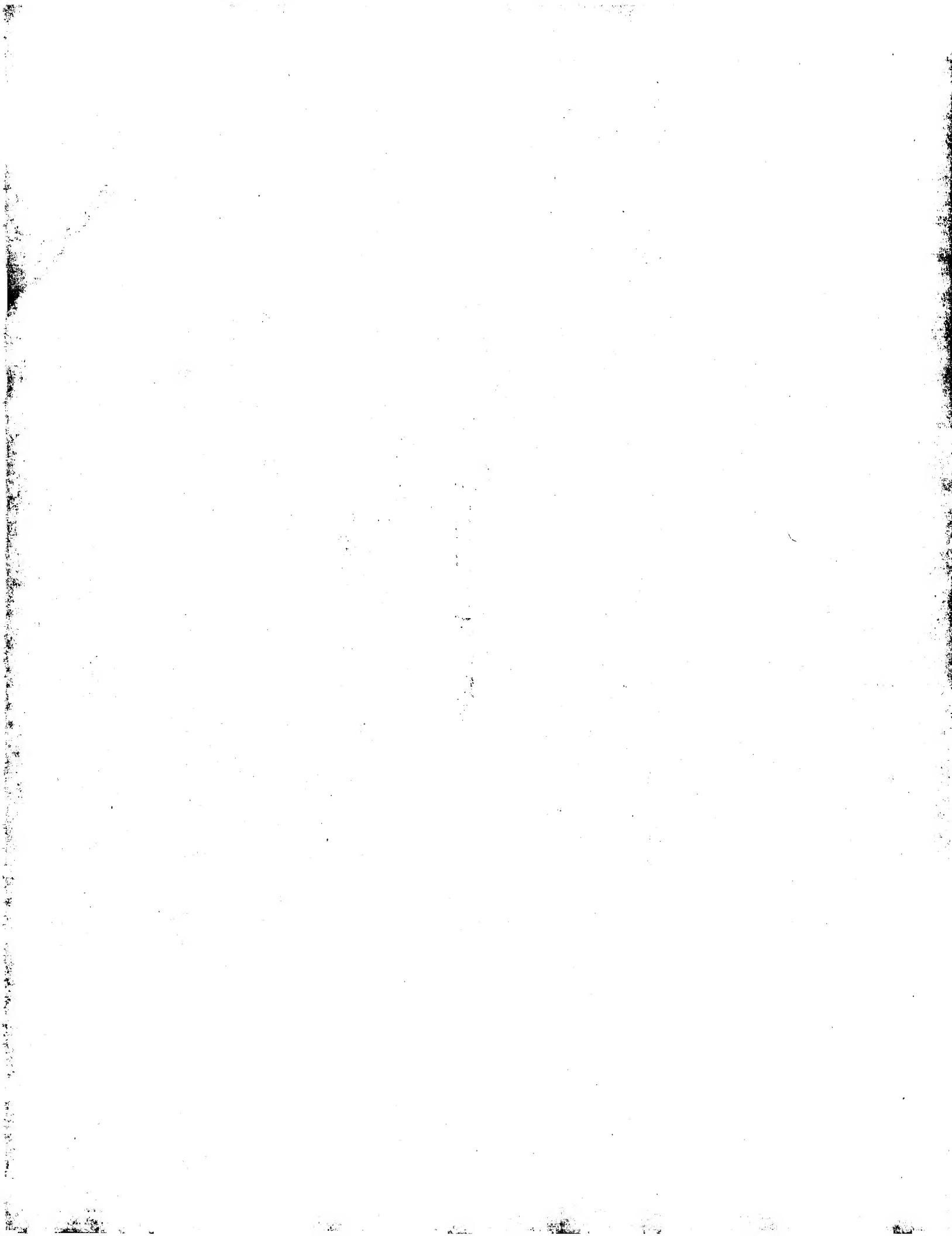
Query Match 100.0%; Score 54; DB 13; Length 39;
Best Local Similarity 18.2%; Pred. No. 71;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

QY	1 CXXXXCXXXXXXXXXXXXCXXXC 22
QY	1 CXXXXCXXXXXXXXXXXXCXXXC 22
Db	5 CAEQCNRRCRGPKPIDCONEHC 26

RESULT 2

Q9VUN2





AC Q60522;
 DT 01-JUL-1997 (TREMBLrel. 04, created)
 DT 023947 PRELIMINARY; PRT; 49 AA.
 ID 023947
 AC 023947;
 DT 01-NOV-1996 (TREMBLrel. 01, created)
 DE 01-NOV-1995 (TREMBLrel. 01, last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 GN ADAM26 OR DTGNA.
 OS MUS musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathli; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10920;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAB/C;
 RX MEDLINE=94195820; PubMed=8146185;
 RA Westkamp G, Blobel C.P.;
 RT "A family of cellular proteins related to snake venom disintegrins."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2748-2751(1994).
 DR EMBL: U06149; AAA1828.1; -.
 DR HSSP: P18619; 1FVL.
 DR MGDB: MGI:105985; Adam26.
 DR INTERPRO: IPR001762; -.
 DR PFAM: PF00200; disintegrin; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR FT NON_TER 1 1
 FT NON_TER 46 46
 SEQUENCE 46 AA; 4950 MW; 9E22D616D43716AC CRC64;
 SQ

Query Match 100.0%; Score 54; DB 11; Length 46;
 Best Local Similarity 18.2%; Pred. No. 78;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXXXXXXXXXXXXXXXXXCXXXC 22
 Db 11 CSSDCVLLKPGAQACAGLCCRN 32

RESULT 6
 09N910 PRELIMINARY; PRT; 47 AA.
 AC 09N910;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Venerupis pullastra.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Venerida;
 OC Veneroidea; Veneridae; Venerupis.
 OX NCBI_TAXID=104387;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GIJL;
 RA Moraga D., Tanduy A.;
 RT "Characterisation of metallothioneins sequences in three clams
 RT Ruditapes decussatus, Ruditapes philippinarum and Venerupis
 RT pullastra.;"
 RT Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AJ2419688; CAB96419.1; -.
 DR FT NON_TER 1 1
 FT NON_TER 47 47
 SEQUENCE 47 AA; 4602 MW; 6FDD54B9126F2B4F CRC64;

Query Match 100.0%; Score 54; DB 5; Length 47;
 Best Local Similarity 18.2%; Pred. No. 79;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

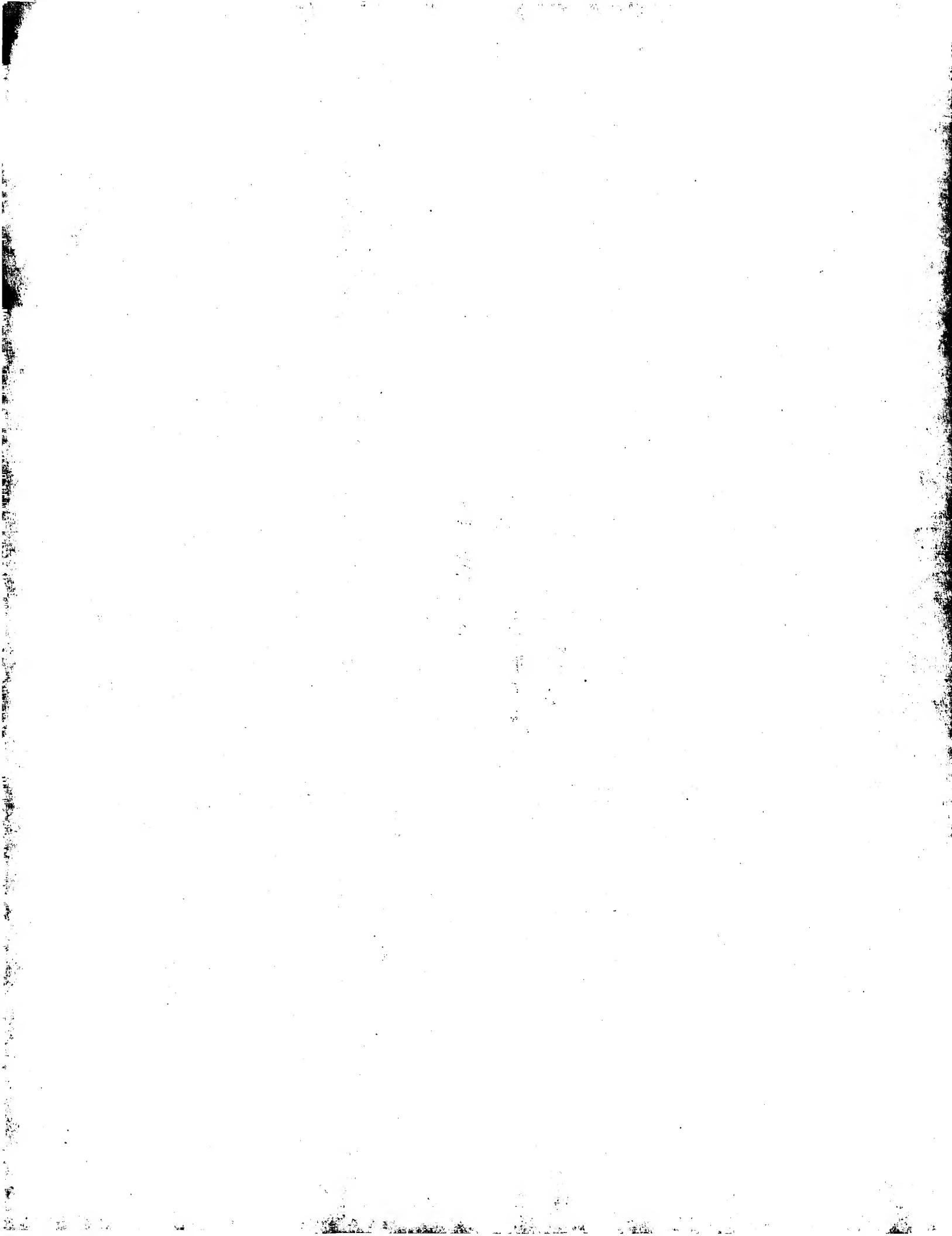
RESULT 7
 023947 PRELIMINARY; PRT; 49 AA.
 ID 023947
 AC 023947;
 DT 01-NOV-1996 (TREMBLrel. 01, created)
 DE 01-NOV-1995 (TREMBLrel. 01, last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 GN DHTC3.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TAXID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuech A., Buenemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/PDBJ databases.
 DR EMBL: X58114; CAA4117.1; -.
 DR FLYBASE: FBgn0015096; DhydMst87Fa.
 DR INTERPRO: IPR001450; -.
 DR PROSITE; PS00196; 4FEAS_FERREDOXIN; UNKNOWN_1.
 DR SEQUENCE 49 AA; 4610 MW; BE158FEC51369F01 CRC64;

Query Match 100.0%; Score 54; DB 5; Length 49;
 Best Local Similarity 18.2%; Pred. No. 81;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 Q23948 PRELIMINARY; PRT; 49 AA.
 ID Q23948
 AC 023948;
 DT 01-NOV-1996 (TREMBLrel. 01, created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE TESTIS SPECIFIC RNA.
 GN DHTC2.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TAXID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuech A., Buenemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: X58114; CAA4118.1; -.
 DR FLYBASE: FBgn0015097; DhydMst87Fb.
 DR INTERPRO: IPR001450; -.
 DR PROSITE; PS00198; 4FEAS_FERREDOXIN; UNKNOWN_1.
 DR SEQUENCE 49 AA; 4550 MW; 24758FEC51369F1D CRC64;

Query Match 100.0%; Score 54; DB 5; Length 49;
 Best Local Similarity 18.2%; Pred. No. 81;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 Q2597 PRELIMINARY; PRT; 49 AA.
 ID Q2597
 AC 02597;
 DR 01-JAN-1998 (TREMBLrel. 05, Created)



DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE METALLOPROTEASE/DISINTEGRIN XNC11.1 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 TISSUE=TUNNIS;
 RX MEDLINE=97349132; PubMed=9205136;
 RA Shilling F.M.; Kratzschmar J.; Cai H.; Weskamp G.; Gayko U.;
 RA Lebow J.; Myles D.G.; Nuccitelli R.; Blobel C.P.;
 RT "Identification of metalloprotease/disintegrins in Xenopus laevis
 RT tests with a potential role in fertilization.";
 RL Dev. Biol. 186:155-164(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TUNNIS;
 RA Kraatzschmar J.; Cai H.; Blobel C.P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 DR HSSP; PI7494; 1KST.
 DR INTERPRO; IPR01762; -.
 DR PF00200; disintegrin; 1.
 DR Integrin; Protease; Metalloprotease.
 FT NON_TER 1 1
 FT NON_TER 49 49
 SQ SEQUENCE 49 AA; 5316 MW; EFBDA4E74DA; 82609 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 49;
 Best Local Similarity 18.2%; Pred. No. 81;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXXCXXC 22
 1 ::::::::::::::::::::|::|:
 Db 13 CCKKCTLSDAMCSGLCCRGC 34

RESULT 10
 ID 008356 PRELIMINARY; PRT; 54 AA.
 AC 008356;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE HIGH-GLYCINE TYROSINE KERATIN TYPE II.3 (FRAGMENT).
 DE KRAF6-3.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 TISSUE=SKIN;
 RA Aoki N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; D89901; BAA19687.1; -.
 DR MGD; MGI:11330279; Krtap-3.
 DR Keratin.
 FT NON_TER 1 1
 SQ SEQUENCE 54 AA; 5729 MW; 2E7880E8822C1787 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 54;
 Best Local Similarity 18.2%; Pred. No. 86;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXXCXXX 22
 1 ::::::::::::::::::::|::|:
 Db 25 CGYGGYGGGGYGGCCSPIC 46

RESULT 11
 ID 09N9H2 PRELIMINARY; PRT; 57 AA.
 AC 09N9H2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE METALLOTHIONEIN (FRAGMENT).
 GN MT.
 OS Ruditapes philippinarum.
 OC Eukaryota; Metaboa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
 OC Veneridae; Veneridae; Ruditapes.
 OX NCBI_TaxID=10434;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Moraga D.; Tanguy A.;
 RT Characterisation of metallothioneins sequences in three clams
 RT Ruditapes decussatus, Ruditapes philippinarum and veneripis
 RT pullastria.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ249686; CAB98403.1; -.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 5411 MW; F7B37567623FD7DD CRC64;

Query Match 100.0%; Score 54; DB 5; Length 57;
 Best Local Similarity 18.2%; Pred. No. 88;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXXXXXCXXC 22
 1 ::::::::::::::::::::|::|:
 Db 12 CSDSCPATGCKCGPGKCGDGC 33

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09U623 PRELIMINARY; PRT; 58 AA.
 ID 09U623
 AC 09U623;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN
 OS Pacificastacus leniusculus (Signal crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Plocoyemata; Astacidea;
 OC Astacoidae; Astacidae; Pacificastacus.
 OX NCBI_TaxID=6720;
 RN [1]
 RP SEQUENCE FROM N.A.
 TISSUE=THORACIC GANGLIA;
 RA Skorupski P.; Dabwani D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF139482; AAF07215.1; -.
 DR HSSP; P55949; 1DMC
 DR INTERPRO; IPR00045; -.
 DR INTERPRO; IPR00019; -.
 DR PFAM; PF00131; metallothionein
 DR PRINTS; PRO00858; MTCRUSTACEAN.
 DR SEQUENCE 58 AA; 6008 MW; 576635ACFB0B5100 CRC64;

Query Match 100.0%; Score 54; DB 5; Length 58;
 Best Local Similarity 18.2%; Pred. No. 89;
 Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXXCXXX 22
 1 ::::::::::::::::::::|::|:
 Db 17 CKTGCVCTSCRCQCDKCTSGC 38

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RESULT	13	AC	Q9VE14;
09N911	PRELIMINARY;	DT	01-MAY-2000 (TREMBLrel. 13, Created)
ID	PRT;	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
09N911;		DE	CG7606 PROTEIN.
RC		GN	Drosophila melanogaster (Fruit fly)
RA	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
RT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	OC	Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
RT		OC	Ephydriidae; Drosophilidae; Drosophila;
RL		OX	NCBI_TAXID=7227;
DR	Ruditapes decussatus.	RN	[1]
EMBL:	AJ249687; CAB96402.1; -	RP	SEQUENCE FROM N.A.
FT		RC	STRAIN-BERKELEY;
FT		RX	MEDLINE=20190006; PubMed=10731132;
FT		RA	Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Roskies R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Heidelberg S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers B.H.C., Blazej R.S., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Bailew R.M., Basu A., Baxendale J., Baykarroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlie C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C., Ferraz C., Farriera S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glässer K., Glocal E., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Bouck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagam C., Jaijai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai C., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosirefi A., Mount S.M., Moy M., Murphy B., Murphy L., Munz Y., Nelson D.M., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacilek J.M., Palazzolo M., Pritchett G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svistak R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasarmian D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Venter J.C.; "The genome sequence of Drosophila melanogaster"; Science 287:2105-2109 (2000).
RA		DR	EMBL: AAF03718; AAF5437.1; -
RA		DR	FLYBASE; FBgn040565; CG6606.
RA		SQ	SEQUENCE 66 AA; 6812 MW; 8151AF9DB3BF85FC CRC64;
RL			Query Match 100.0%; Score 54; DB 10; Length 62;
DR			Best Local Similarity 18.2%; Pred. No. 93; Mismatches 4;保守性 18; Indels 0; Gaps 0;
DR			Matches 4; Conservat 18; Mismatches 0; Indels 0; Gaps 0;
DR			NON-TER 1
FT	SEQUENCE 62 AA; 6886 MW;		A576222C14631F35 CRC64;
FT			Query Match 100.0%; Score 54; DB 5; Length 66;
FT			Best Local Similarity 18.2%; Pred. No. 96; Mismatches 4;保守性 18; Indels 0; Gaps 0;
FT			Matches 4; Conservat 18; Mismatches 0; Indels 0; Gaps 0;
QY	1 CXXCXXXXXXXXXXXXCXXC 22	QY	1 CXXCXXXXXXXXXXXXCXXC 22
Db	4 CGGCGSYRCSATSHKPCMFCC 25	Db	30 CGCGCGKPCQCLSCGSRSGCGC 51

Query Match 100.0%; Score 54; DB 10; Length 62;
 Best Local Similarity 18.2%; Pred. No. 93;
 Matches 4; Conservat 18; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXXXXXXXCXXC 22
 Db 4 CGGCGSYRCSATSHKPCMFCC 25

Search completed: March 1, 2001, 16:22:09
 Job time: 286 sec

RESULT 15
 Q9VE14 PRELIMINARY; PRT; 66 AA.

